

Figure 1

10 30 50
 CACGCGTCCGCGGGCGCGGCCGAGAACCCCGCAATCTTTGCGCCACAAAATACACCGA
 70 90 110
 CGATGCCCGATCTACTTTAAGGGCTGAAACCCACGGGCTGAGAGACTATAAGAGCGTTC
 130 150 170
 CCTACCGCCATGGAACAACGGGGACAGAACGCCCCGGCCGCTTCGGGGGGCCCGGAAAAGG
M E O R G O N A P A A S G A R K R
 190 210 230
 CACGGCCAGGACCCAGGGAGGCGCGGGGAGCCAGGCCTGGGCCCCGGGTCCCCAAGACC
H G P G P R E A R G A R P G P R V P K T
 250 270 290
 CTTGTGCTCGTTGTGCGCCGCGGTCTGCTGTTGGTCTCAGCTGAGTCTGCTCTGATCACC
L V L V V A A V L L L V S A E S A L I T
 310 330 350
 CAACAAGACCTAGCTCCCCAGCAGAGAGCGGCCCCACAACAAAAGAGGTCCAGCCCCCTCA
 Q Q D L A P Q Q R A A P Q Q K R S S P S
 370 390 410
 GAGGGATTGTGTCCACCTGGACACCATATCTCAGAAGACGGTAGAGATTGCATCTCCTGC
 E G L C P P G H H I S E D G R D C I S C
 430 450 470
 AAATATGGACAGGACTATAGCACTCACTGGAATGACCTCCTTTTCTGCTTGCGCTGCACC
 K Y G Q D Y S T H W N D L L F C L R C T
 490 510 530
 AGGTGTGATTGAGGTGAAGTGGAGCTAAGTCCCTGCACCACGACCAGAAACACAGTGTGT
 R C D S G E V E L S P C T T T R N T V C
 550 570 590
 CAGTGCGAAGAAGGCACCTTCCGGGAAGAAGATTCTCCTGAGATGTGCCGGAAGTGCCGC
 Q C E E G T F R E E D S P E M C R K C R
 610 630 650
 ACAGGGTGTCCCAGAGGGATGGTCAAGGTCCGGTGATTGTACACCCTGGAGTGACATCGAA
 T G C P R G M V K V G D C T P W S D I E
 670 690 710
 TGTGTCCACAAAGAATCAGGCATCATATAGGAGTCACAGTTGCAGCCGTAGTCTTGATT
C V H K E S G I I I G V T V A A V V L I
 730 750 770
 GTGGCTGTGTTTGTGTTGCAAGTCTTTACTGTGGAAGAAAGTCCTTCCTTACCTGAAAGGC
V A V F V C K S L L W K K V L P Y L K G
 790 810 830
 ATCTGCTCAGGTGGTGGTGGGGACCCTGAGCGTGTGGACAGAAGCTCACAAACGACCTGGG
 I C S G G G G D P E R V D R S S Q R P G
 850 870 890
 GCTGAGGACAATGTCCTCAATGAGATCGTGAGTATCTTGCAGCCACCCAGGTCCCTGAG
 A E D N V L N E I V S I L Q P T Q V P E
 910 930 950
 CAGGAAATGGAAGTCCAGGAGCCAGCAGAGCCAACAGGTGTCAACATGTTGTCCCCCGGG
 Q E M E V Q E P A E P T G V N M L S P G
 970 990 1010
 GAGTCAGAGCATCTGCTGGAACCGGCAGAAGCTGAAAGGTCTCAGAGGAGGAGGCTGCTG
 E S E H L L E P A E A E R S Q R R R L L
 1030 1050 1070

Figure 1 (continued)

GTTCCAGCAAATGAAGGTGATCCCACTGAGACTCTGAGACAGTGCTTCGATGACTTTGCA
V P A N E G D P T E T L R Q C F D D F A
1090 1110 1130
GACTTGGTGCCCTTTGACTCCTGGGAGCCGCTCATGAGGAAGTTGGGCCTCATGGACAAT
D L V P F D S W E P L M R K L G L M D N
1150 1170 1190
GAGATAAAGGTGGCTAAAGCTGAGGCAGCGGGCCACAGGGACACCTTGTACACGATGCTG
E I K V A K A E A A G H R D T L Y T M L
1210 1230 1250
ATAAAGTGGGTCAAACAAAACCGGGCGAGATGCCTCTGTCCACACCCTGCTGGATGCCTTG
I K W V N K T G R D A S V H T L L D A L
1270 1290 1310
GAGACGCTGGGAGAGAGACTTGCCAAGCAGAAGATTGAGGACCCTTGTGAGCTCTGGA
E T L G E R L A K Q K I E D H L L S S G
1330 1350 1370
AAGTTCATGTATCTAGAAGGTAATGCAGACTCTGCCATGTCCTAAGTGTGATTCTCTTCA
K F M Y L E G N A D S A M S *
1390 1410 1430
GGAAGTGAGACCTTCCCTGGTTTACCTTTTTTCTGGAAAAAGCCCAACTGGACTCCAGTC
1450 1470 1490
AGTAGGAAAGTGCCACAATTGTCACATGACCGGTACTGGAAGAACTCTCCCATCCAACA
1510 1530 1550
TCACCCAGTGGATGGAACATCCTGTAACCTTTTCACTGCACTTGGCATTATTTTATAAGC
1570 1590
TGAATGTGATAATAAGGACACTATGGAAAAAAAAAAAAA

Figure 2

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1  M-LG-----I W T L L P L V L h Fas protein
1  E G L S-----T V P D L L L P L h TNFR I Protein
1  H S Q R-----B R G C A A V A A DR3 protein
1  H E Q R C Q N A P A A S G A R K R H G P G P R E A R G A R P G P R V P K T L V L HLYBX88XXprotein

13 T S V R L S S K S V N A Q V T D I N S K G L E L R K T V T T V E T Q N L E G L h Fas protein
14 V P L E L L V G I Y P S G V I G L V P H L G D R E K R D S V C P Q G X Y I H-- h TNFR I Protein
14 A E L E L L L G A R A Q G-----G T R S P R-C D C A-G D F-H-- DR3 protein
41 V T A A V L L L V S A S A L I T Q Q D L A P Q Q R A A P Q Q K R S S P S E G L HLYBX88XXprotein

53 H E D G Q E C H K P C P P G E R K A R D C T V N G D E P D C V P C Q E G K E V T h Fas protein
52 P Q N N S C C T K C H K G T Y L Y N D C P G P G Q D T D C R E C E S G S F T A h TNFR I Protein
41 K X I G L E C C R G C P A G H Y L K A P C T E P C G N S T C L V C P Q D T F L A DR3 protein
81 -----C P P G E H I S E D-----G R D C I S C K Y E Q D Y S HLYBX88XXprotein

93 D K A H F S S K C R R C R L C D E G H G L E V E I N C T R T Q N T K C R C K P N h Fas protein
92 S E N H L 2-H C L S C S K C R K E M G Q V E I S S C T V D R D T V C G C R K N h TNFR I Protein
81 W E N H H W S E C A R C Q A C D E Q A S O V A L E N C S A V A D T R C G C K P G DR3 protein
105 T E W N D L L F C L R C T R C D--S G E V E L S F C T T T R N T V C Q C E E G HLYBX88XXprotein

133 F E-----C N S T V-----C E H C D P C T K----- h Fas protein
131 Q Y R E H Y W S E N L F Q C-----F N C S L C L N-G T V H-----L S C Q E h TNFR I Protein
121 W E V E C-----Q V S O C V S S S P F Y C Q P C L D C G A L H R H T R L L C S R DR3 protein
143 T F R P-----E D S P E M C R K C-----R T G C P R HLYBX88XXprotein

149 -----C E H G I I-----K E C-----T L T S N T K C K E----- h Fas protein
161 K Q N T V C T C H A G F F L R E N E C V S C S N C K K S E C T E L C L P Q F E h TNFR I Protein
158 R D T D C G T C L E G E Y Z H G D G C V S C P T S T L G-S C P E R C A A V C G DR3 protein
163 G M V K V G D C T E-----W S D I E C V-----H R E S G I I E G HLYBX88XXprotein

168 -----E G S R S N L G W-----L C L L-L L P I P L I V-----W h Fas protein
201 N Y K G T E D S G C T V L L P L V I S F G E C L L S L L F I G L M Y R Y Q R-W h TNFR I Protein
197 W R Q-----M F W V Q V L L A G E L V V P L L E G A T L T Y T Y R H C W DR3 protein
189 -----V T V A A V V L I V A V E--V C K S L L W K K V L E Y L K G I C S HLYBX88XXprotein

190 V E R R E V Q K F C R R H E K E N Q G S H E S----- h Fas protein
240 -E S R L Y S I V C G R S T P E K Z G E L E G T T T K P L A P N P S F S P T P G h TNFR I Protein
229 -P H R P L-V F A D E A G M E A L T P P P A T H L S E L D S A H T L L A B P D DR3 protein
221 -----G G G G D P E R V D R S S Q R P G A E D N V E N E I V S I L Q P T Q HLYBX88XXprotein

213 ----- h Fas protein
279 F T P C L G F S P V P S S T F T S S S Y T F P G D-C P N F A A P R R E V A P P h TNFR I Protein
267 S S E K I C T V Q L V G N S W E P G Y P E T Q E A L C E Q V T W S W D Q L--P DR3 protein
255 V P E Q E M E V O E P A E-----P T G V N M L S P G-----E S E H L-- HLYBX88XXprotein

213 -----E T L N E E T V A I N L--S D V D L S K Y I T T I A G V M h Fas protein
313 Y Q G A D P I L A T A L A S D P I P N P L Q K W E D S A H K P Q S L D T D D P A h TNFR I Protein
305 S R A L G P A A A E T E S E-----E S P A G S P A M M L Q P G P Q DR3 protein
283 -----L E P A E A E R S Q R R R L L V P A N E G D P T E T L R O HLYBX88XXprotein

241 T E S Q V-----E G E V R R N G V N E A K I D E I K N D N V Q D T A h Fas protein
359 T E Y A V V E N V E P L R W K E F V R L G L S D R E I D R L E L Q M C R C L R h TNFR I Protein
335 -L Y D V M D A V P A R R W K E F V R L G L R E A E I E A V E V E I G R-F R DR3 protein
312 C E D D F A D L V E P D S E P L M E R L G L M D N E T-K V A K A E A A G H R HLYBX88XXprotein

272 E O K V Q L L R N H O L H G K K E A-Y D T L I K D E K K A N L C T L A E K I h Fas protein
398 E A Q Y S M L A T E R R R T P R R E A T L E L L G R V L R D M D L L G C L E D T h TNFR I Protein
373 D O O Y E M I K R E R O Q Q P--A G L G A V Y A A L E R M G L D G C V E D L DR3 protein
351 D T L V T M L I K M V N K T G P-D A S V H T L L D A L E T L G E R L A K Q K I HLYBX88XXprotein

311 Q T I I L K D I T S D S E N S W E R N E I Q S L V h Fas protein
438 E E A E-----C G P A A L P P A P S L L R h TNFR I Protein
415 -----R S R L Q R G P DR3 protein
390 E D H E L S S G K F M Y L E G M--A D S A M S HLYBX88XXprotein

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Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.

Figure 3

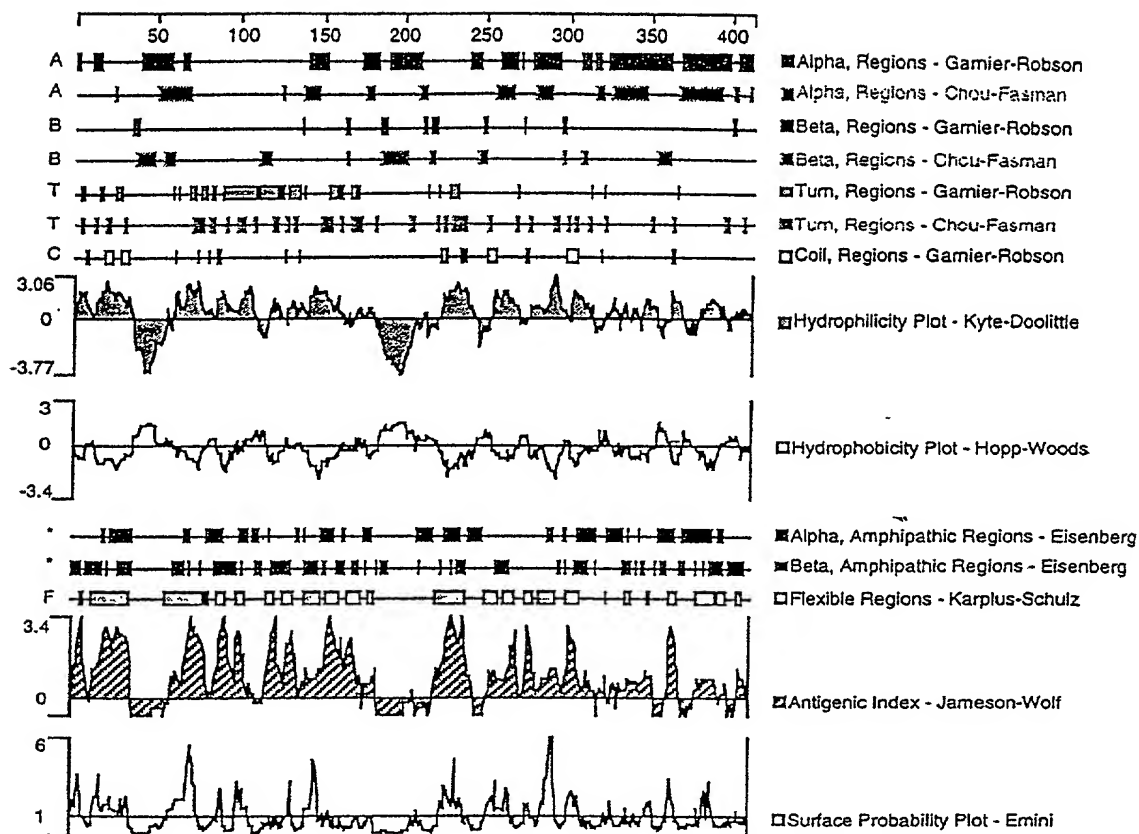


Figure 4

HAPBU13R

1 AATTCGGCAC AGCTCTTCAG GAAGTCAGAC CTTCCCTGGT TTACCTTTTT
51 TCTGGAAAAA GCCCAACTGG GACTCCAGTC AGTAGGAAAG TGCCACAATT
101 GTCACATGAC CGGTACTGGA AGAAACTCTC CCATCCAACA TCACCCAGTG
151 GNATGGGAAC ACTGATGAAC TTTTCACTGC ACTTGGCATT ATTTTTGTNA
201 AGCTGAATGT GATAATAAGG GCACTGATGG AAATGTCTGG ATCATTCCGG
251 TTGTGCGTAC TTTGAGATTT GNGTTTGGGG ATGTNCATTG TGTTTGACAG
301 CACTTTTTTN ATCCCTAATG TNAAATGCNT NATTTGATTG TGANTTGGGG
351 GTNAACATTG GTNAAGGNTN CCCNTNTGAC ACAGTAGNTG GTNCCCGACT
401 TANAATNGNN GAANANGATG NATNANGAAC CTTTTTTTGG GTGGGGGGGT
451 NNCGGGGCAG TNNAANGNNG NCTCCCCAGG TTTGGNGTNG CAATNGNGGA
501 ANNNTGG

HSBBU76R

1 TTTTTTTTGT AGATGGATCT TACAATGTAG CCCAAATAAA TAAATAAAGC
51 ATTTACATTA GGATAAAAAA GTGCTGTGAA AACAATGACA TCCCAAACCA
101 AATCTCAAAG TACGCACAAA CGGAATGATC CAGACATTC CATAGNGTCC
151 TTATTATCAC ATTCAGCTTA TAAAANTAAT GCCAAGTGCA GTGAAAAGTT
201 ACAGGATGTT CCATCCACTG GGTGGATT

Figure 5

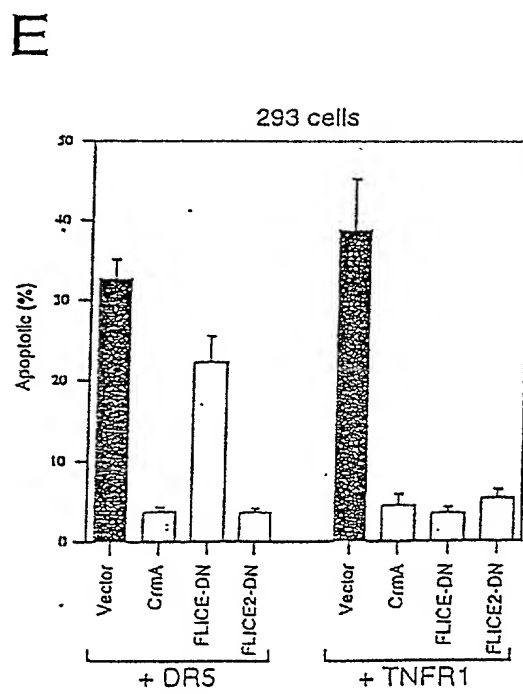
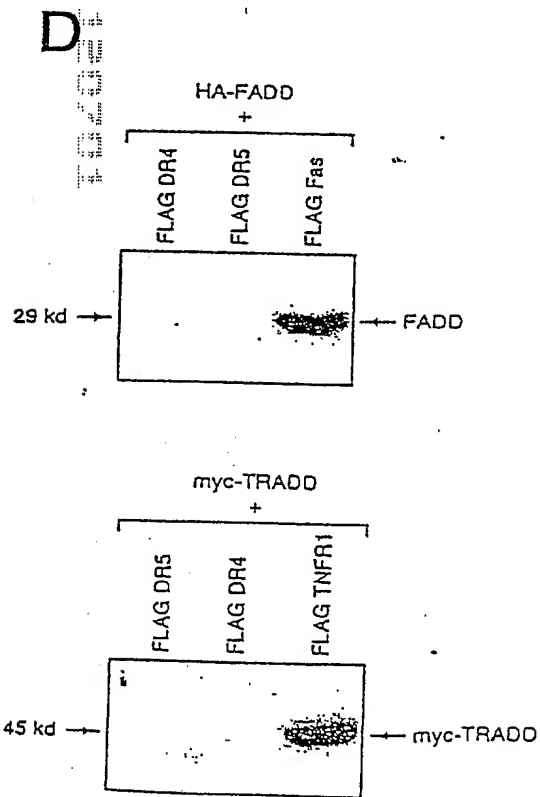
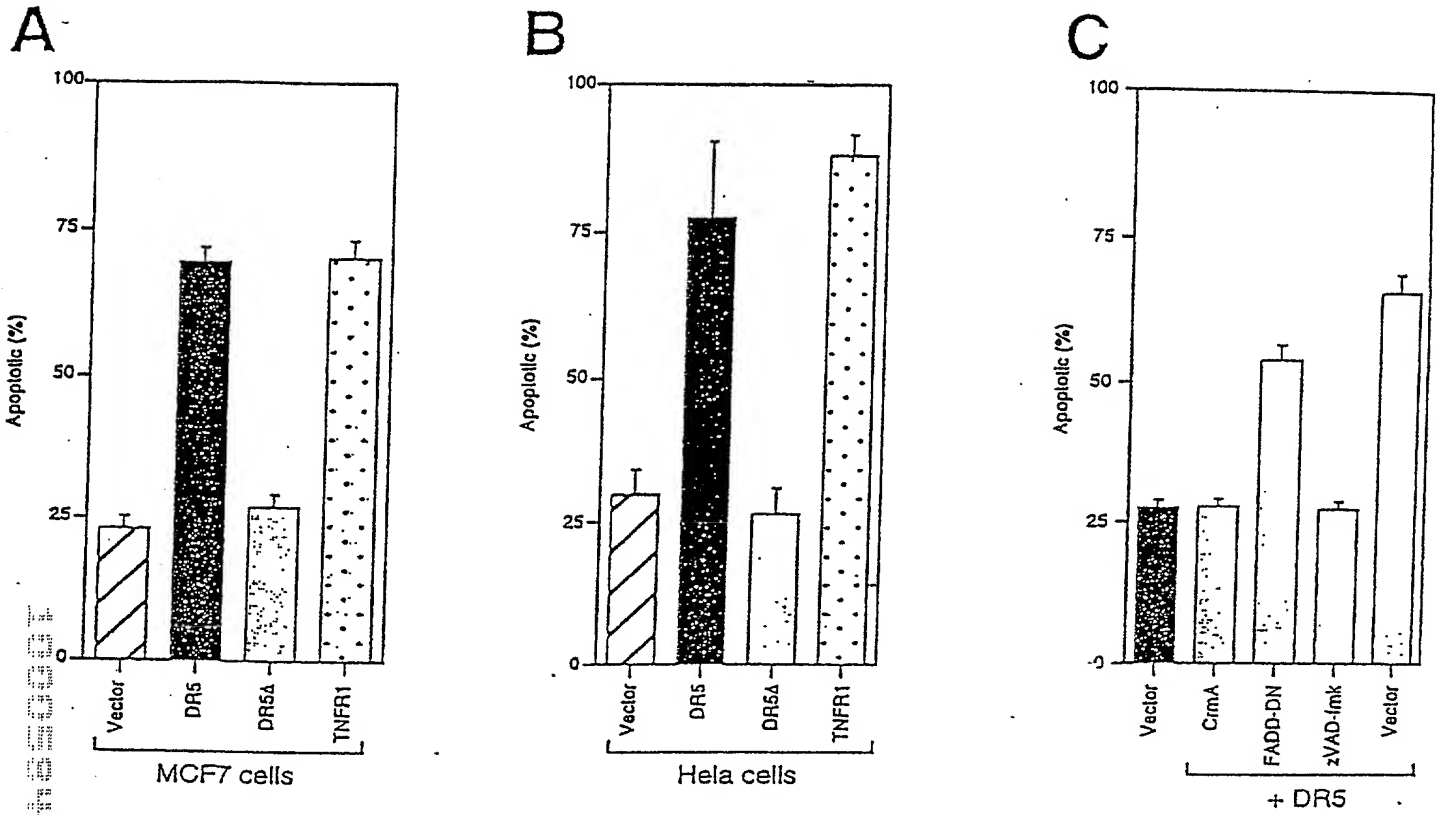
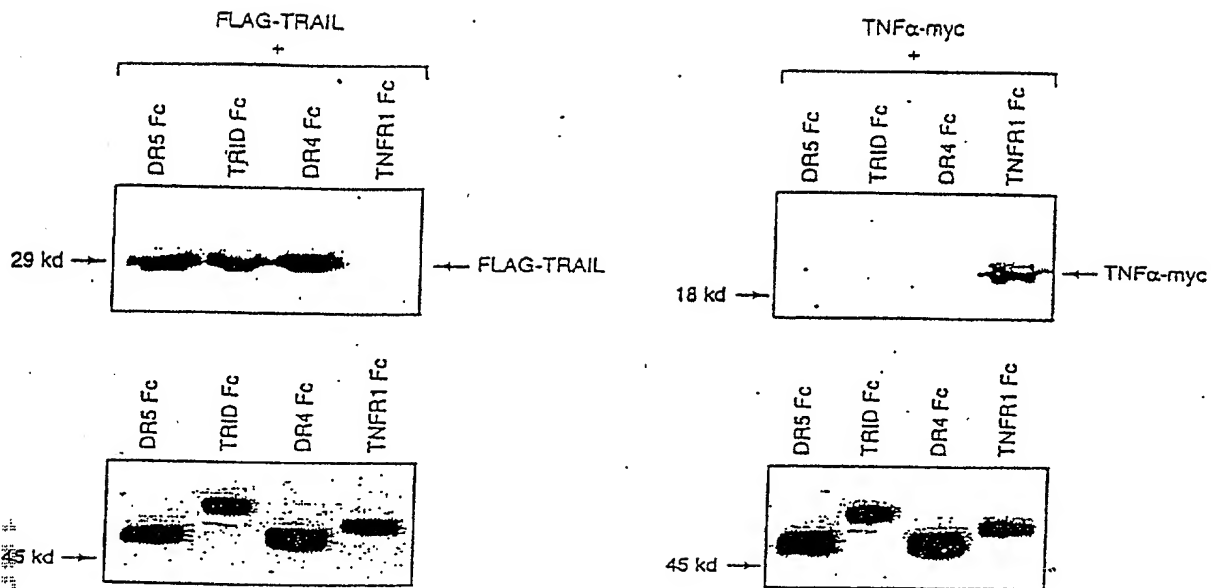
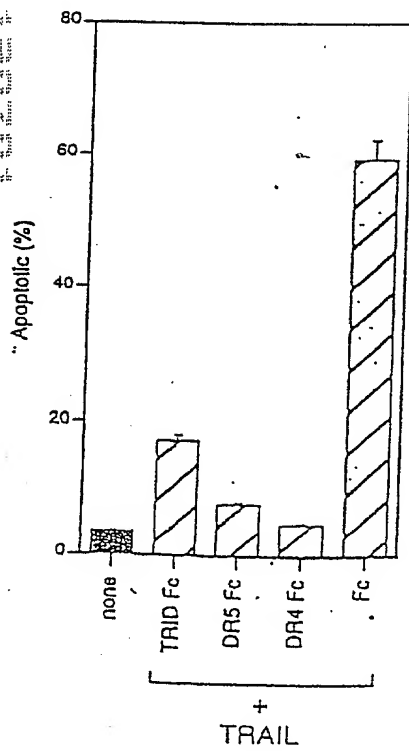


Figure 6

A



B



C

